

SEQUENCE LISTING

<110> The University of Georgia Research Foundation, Inc

<120> A POLYPEPTIDE HAVING AMIDOLYTIC ACTIVITY FOR A SERPIN

<130> 235.00210201

<140> PCT/US00/10574

<141> 2000-04-20

<150> 60/130,436

<151> 1999-04-21

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 843

<212> PRT

<213> Porphyromonas gingivalis

<400> 1

Met Lys Lys Ser Phe Leu Leu Ala Ile Val Met Leu Phe Gly Ile Ala
1 5 10 15

Met Gln Gly His Ser Ala Pro Val Thr Lys Glu Arg Ala Leu Ser Leu
20 25 30

Ala Arg Leu Ala Leu Arg Gln Val Ser Leu Arg Met Gly Gln Thr Ala
35 40 45

Val Ser Asp Lys Ile Ser Ile Asp Tyr Val Tyr Arg Gln Gly Asp Ala
50 55 60

Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly Ser Pro Ala Tyr Phe Tyr
65 70 75 80

Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr Ala Leu Val Ala Ala Asp
85 90 95

Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser Pro Ile Gly Arg Phe Asp
100 105 110

Met Asp Ser Met Pro Asp Asn Leu Arg Met Trp Leu Gln Ile Tyr Asp
115 120 125

10030330-101901

Tyr Gln Glu Ile Ile Thr Gly Ile Glu Pro Ala Lys Thr Pro Ala Glu
385 390 395 400

Ala Gly Thr Asp Ala Leu Pro Ile Leu Ala Leu Lys Asp Ile Glu Ala
405 410 415

Glu Tyr Lys Ser Glu Ser Gly Leu Asn Val Gly Tyr Ser Ile Tyr Asn
420 425 430

Thr Gly Glu Glu Gln Ser Asn Leu Asp Leu Gly Tyr Arg Leu Asn Lys
435 440 445

Ala Asp Gly Glu Val Ile Glu Val Lys Thr Ser Ser Ile Asn Ile Ser
450 455 460

Trp Tyr Gly Tyr Gly Glu His Pro Glu Ser Phe Ser Leu Ala Pro Asn
465 470 475 480

Gln Leu Ser Gln Gly Ile Asn Thr Ile Thr Leu Leu Tyr Arg Arg Thr
485 490 495

Gly Thr Glu Gln Trp Glu Pro Val Arg His Ala Gln Gly Gly Tyr Val
500 505 510

Asn Ser Ile Lys Val Asn Thr Thr Asp Pro Asn Asn Val Val Val Thr
515 520 525

Val Asp Asn Asn Glu Gly Lys Leu Ser Ile Val Pro Asn Ser Phe Val
530 535 540

Ala Asp Leu Asn Ser Tyr Glu His Ser Thr Ile Thr Val Gln Phe Asn
545 550 555 560

Ser Asp Ser Pro Asp Glu Ile Arg Thr Pro Val Ala Phe Ala Leu Ser
565 570 575

Thr Gly Ala Thr Ala Asp Asp Val Ile Ser Leu Gly Trp Val Met Ala
580 585 590

Glu Val Pro Gly Gly Ser Ser Asn Tyr Pro Val Val Trp Ser Lys Asp
595 600 605

Val Leu Thr Leu Ser Glu Gly Asp Tyr Thr Leu Trp Tyr Arg Phe Ser
610 615 620

Ile Asn Asn Gln Lys Asp Glu Trp Lys Lys Ile Gly Ser Val Ser Val
625 630 635 640

Lys Thr Pro Thr Glu Tyr Thr His Pro Leu Phe Glu Val Gly His Asn
645 650 655

Gln Thr Ser Thr Tyr Thr Leu Asp Met Ala His Asn Arg Val Leu Pro
660 665 670

Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro Phe Asn Gly Glu Leu Val
675 680 685

Val Val Phe Arg Gln Thr Gln Ser Ser Ser Gly Ser Leu Trp Ala Ala
690 695 700

Gln Glu Thr Val His Ile Lys Gln Gly Glu Thr Phe Val Tyr Lys Pro
705 710 715 720

Val Val Glu Gly Pro Ile Pro Asp Gly Ser Tyr Arg Ala Thr Leu His
725 730 735

Ala Phe Val Asn Gly Gln Gln Gln Leu Tyr Leu Lys Gly Lys Arg Asn
740 745 750

Tyr Thr Val Lys Ile Val Asn Gly Thr Ala Val Glu Ala Ile Glu Ser
755 760 765

Ser Glu Glu Ile Arg Val Phe Pro Asn Pro Ala Arg Asp Tyr Val Glu
770 775 780

Ile Ser Ala Pro Cys Ile Pro Gln Glu Thr Ser Ile Ile Leu Phe Asp
785 790 795 800

Leu Ser Gly Lys Ile Val Met Lys Asn Ser Leu Ser Ala Gly His Gly
805 810 815

Arg Met Asp Val Ser Arg Leu Pro Asn Gly Ala Tyr Ile Leu Lys Val
820 825 830

Asp Gly Tyr Thr Thr Lys Ile Asn Ile Val His
835 840

<210> 2

<211> 2532

<212> DNA

<213> Porphyromonas gingivalis

<400> 2

atgaaaaaaa gttttctttt agccatagta atgctctttg gcattgccat gcagggacat 60
tctgctccgg ttacgaaaga gcgagctttg agtctggctc ggctggcttt gcgacaggta 120

tcc	ttgc	gcaa	tggg	acaaac	agcag	tatct	gaca	agattt	ccat	cagatta	cgttt	atcgg	180
caagg	agatg	ctgag	agggg	tatcac	atca	caagg	aggaag	gctct	cctgc	atattt	tttat	240	
gtagc	taatc	gtgg	aaataa	tgagg	gctat	gctct	ttgtag	cagc	agatga	caga	ataccg	300	
acaatt	tttag	cctatt	cacc	cattg	gccgt	ttcg	acatgg	acagt	atgcc	ggaca	aatctt	360	
cgcat	gtggc	tacaa	atttta	cgatc	aggaa	atagg	gcctga	tacttt	ccgg	aaaag	ctcag	420	
ctcaat	gaag	agatatt	acg	taccg	agggc	gtacc	ggctg	aagt	acatgc	tctga	tggat	480	
aacggt	catt	ttgcca	acga	tcccat	gcga	tgg	aatcaag	gttacc	ccatg	gaaca	ataag	540	
gaacc	actgc	ttccta	aatgg	caatc	atgcc	tatac	ccggct	gtgtt	gctac	tgctg	cagca	600	
caaat	catgc	gctacc	atag	ctggc	cgctt	caagg	tgaag	gctct	ttcga	ttatc	atgca	660	
ggttc	attag	ttggc	aactg	gtccg	gcaca	tttgg	tgaaa	tgtac	gactg	gatca	aatatg	720	
cccgg	aaatc	ccgac	cttga	taatc	tgact	caatc	tcaag	tggat	gccta	cgcc	acactg	780	
atg	cgtgatg	tgagt	gcac	tgttt	cgatg	agttt	ttatg	aaaat	ggaag	tggta	cgta	840	
agcgt	tttatg	tagta	ggagc	cttgc	gaaac	aactt	tcgct	acaag	cgttc	actgc	cagcta	900	
catgt	acgcg	ccttat	atatac	ctcac	aggag	tggc	acgata	tgatc	cgcg	ggaac	ttgcc	960	
tccgg	aaggc	cggct	ctatta	tgcag	ggaat	aacc	agagca	tagga	catgc	tttcg	tttgc	1020	
gatg	gttatg	cttc	ggatgg	tactt	ccat	ttca	actggg	gttgg	ggagg	tgttt	ccaac	1080	
ggctt	ctaca	aacta	acact	cctct	cgcg	acttc	gttg	gtatc	ggagg	tgagg	gaata	1140	
ggttt	tacca	tttat	caaga	gatca	tcacc	ggtat	cgaac	cggct	aaagac	tccc	gctgaa	1200	
gccg	gtacag	atgc	ccttgcc	gatct	tggca	ctg	aaagaca	taga	agccga	gtata	aaaagt	1260	
gaatc	cggat	tga	acgtagg	gtatt	cgata	tata	atacag	gtga	agagca	atcaa	atctt	1320	
gacct	cggat	acaga	ttgaa	caagg	ctgac	ggaga	agtc	taga	ggtgaa	aactt	catct	1380	
atca	atatct	cttgg	tacgg	atac	ggagag	catcc	cgaga	gtttc	tcat	ggcac	cta	1440	
cag	ttgtcac	aagga	atcaa	cacc	atcacc	ctact	ttatc	gtcgc	acag	caccg	aacag	1500	
tggg	agccgg	tacgg	catgc	acagg	gagga	tatgt	caata	gcatt	aaagt	aaata	cagaca	1560	
gaccc	gaaca	atgtc	gtagt	cacg	gtagat	aata	acgaag	gcaag	ctcag	tatcg	tccc	1620	
aacag	ccttg	tcgc	agatct	gaatt	ctttat	gaac	atagta	cgatt	acagt	acagt	tcaat	1680	
agc	gacagcc	ctgat	gagat	ccgt	acaccc	gtag	cctttg	ctct	atctac	aggag	ctact	1740	
gcgg	acgatg	taat	atcttt	ggg	ctgggt	atgg	ctgaag	ttcc	ggcg	tagc	agcaac	1800	
tatc	cggtgg	tttgg	tctaa	agac	gttctc	actc	ctcgcg	aagg	cgact	tac	attgtg	1860	
tata	gatttt	ccat	caacaa	ccaaa	aggat	gaat	ggaaaa	agat	cggaa	cgtgt	cagta	1920	
aaa	acaccga	cagag	tatac	gcac	ccctta	ttcg	aagtgg	gcc	ataatca	aactt	ctacc	1980	
tata	cgcctgg	atat	ggcaca	caac	agagta	ttg	cccga	ctac	actcaa	aaatc	tcgga	2040	
ttgc	cctttca	atgg	tga	gtt	gttgtt	ttcc	gcaaaa	caca	atcctc	atc	gggtct	2100	
ttat	gggcag	ctca	agaaac	agt	acatatc	aag	caaggag	aaact	ttcgt	atata	aacct	2160	
gttg	tgcgaag	gcc	ctatacc	tga	tggatcc	tat	cgtgcga	ccct	ccatgc	attc	gtaa	2220	
ggaca	acaac	agtt	gtacct	caagg	gggaaa	agga	actaca	cgtg	gaagat	cgt	caatggt	2280	
acag	cggtag	aag	caataga	atcgt	cagaa	gag	atcagag	tatt	ccctaa	tcc	ggcacgc	2340	
gatt	atgtgg	aaat	atcggc	acct	tgcat	cccc	aagaaa	cat	ctatcat	tctt	ttcgat	2400	
ctgt	caggca	agatt	gtcat	gaaga	aatagt	ttat	cagcgg	ggc	atggcag	aat	ggatgtc	2460	
agcc	gacttc	cta	atggggc	ctaca	tcctt	aagg	tggatg	gat	atac	gac	gaaa	ataat	2520
ata	gtg	cact	aa										2532</

```
<210> 3
<211> 418
<212> PRT
<213> Homo sapiens
```

<400> 3

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
1 5 10 15

Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
20 25 30

Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
35 40 45

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
50 55 60

Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
65 70 75 80

Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
85 90 95

His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
100 105 110

Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
115 120 125

Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
145 150 155 160

Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
165 170 175

Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
180 185 190

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
195 200 205

Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
210 215 220

Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
225 230 235 240

Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
245 250 255

10030330 101901



Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
260 265 270

Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
275 280 285

Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
290 295 300

Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
305 310 315 320

Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
325 330 335

Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
340 345 350

Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
355 360 365

Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
370 375 380

Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
385 390 395 400

Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
405 410 415

Gln Lys

<210> 4
<211> 15
<212> PRT
<213> Homo sapiens

<400> 4
Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu
1 5 10 15

<210> 5
<211> 840
<212> PRT

<213> Porphyromonas gingivalis

<400> 5

Met Lys Arg Ile Phe Tyr Thr Leu Gly Leu Leu Leu Leu Cys Leu Pro
1 5 10 15

Met Leu Gln Ala Gly Pro Val Thr Arg Ser Lys Ala Glu Gln Thr Ala
20 25 30

Lys Asn Phe Phe Ala Lys Arg Gln Pro Thr Leu Ser Ser Ser Thr Ala
35 40 45

Ser Leu Arg Met Asp Phe Val Tyr Lys Ala Ala Glu Arg Glu Glu Ala
50 55 60

Leu Phe Phe Val Phe Asn Arg Gly Glu Lys Asp Gly Phe Leu Leu Val
65 70 75 80

Ala Ala Asp Asp Arg Phe Pro Glu Val Ile Gly Tyr Ala Phe Lys Gly
85 90 95

His Phe Asp Ala Ala Arg Ile Pro Asp Asn Leu Arg Gly Trp Leu Lys
100 105 110

Gly Tyr Glu Arg Glu Met Leu Ala Val Met Asp Gly Lys Ala Glu Pro
115 120 125

Ile Asp Pro Ile Arg Glu Ala Lys Pro Thr Arg Asp Leu Pro Ser Ser
130 135 140

Ile Ala Pro Ile Leu Glu Thr Gly Glu His Ala Ser Asp Pro Ile Leu
145 150 155 160

Trp Asp Gln Gly Tyr Pro Phe Asn Thr Leu His Pro Leu Leu Pro Ser
165 170 175

Gly Gln Gln Ala Tyr Thr Gly Cys Val Ala Thr Ala Met Gly Gln Ile
180 185 190

Met Arg His Tyr Lys Trp Pro Glu Lys Ala Ser Gly Glu Tyr Asp Tyr
195 200 205

Tyr Asp Asp Met Thr Gly Thr His Thr His Tyr Ser Gly Thr Phe Gly
210 215 220

Glu Thr Tyr Asn Trp Ser Lys Met Pro Gly Asn Ile Ser Val Gly Ile
225 230 235 240

Ser	Pro	Glu	Glu	Val	Lys	Ala	Leu	Ser	Thr	Phe	Met	Arg	Asp	Val	Ser	
				245					250					255		
Phe	Ser	Val	Asn	Met	Gln	Phe	Ala	Asp	Phe	Gly	Ser	Gly	Thr	Phe	Ser	
				260					265					270		
Ile	Phe	Val	Glu	Arg	Ala	Leu	Arg	Glu	Thr	Phe	His	Tyr	Lys	Lys	Ser	
				275					280					285		
Leu	Arg	Tyr	Ile	His	Arg	Ser	Leu	Leu	Pro	Gly	Lys	Glu	Trp	Lys	Asp	
				290					295					300		
Met	Ile	Arg	Lys	Glu	Leu	Ala	Glu	Asn	Arg	Pro	Val	Tyr	Tyr	Ala	Gly	
305					310					315					320	
Ala	Asp	Gly	Ser	Met	Gly	His	Ala	Phe	Val	Cys	Asp	Gly	Tyr	Glu	Pro	
				325					330					335		
Asp	Gly	Thr	Phe	His	Phe	Asn	Trp	Gly	Trp	Gly	Gly	Met	Ser	Asn	Gly	
				340					345					350		
Asn	Phe	Tyr	Leu	Asn	Leu	Leu	Asn	Pro	Gly	Ser	Leu	Gly	Thr	Arg	Ala	
				355					360					365		
Gly	Asp	Gly	Gly	Tyr	Ser	Thr	Asp	Gln	Glu	Val	Val	Ile	Gly	Ile	Glu	
				370					375					380		
Pro	Ala	Ser	Asn	Glu	Val	Pro	Gly	Ile	Val	Pro	Asp	Pro	Thr	Ile	Thr	
385					390					395					400	
Leu	Tyr	Gly	Leu	Gln	His	Asn	Met	Ser	Asp	Glu	Ala	Leu	Asp	Leu	Ser	
				405					410					415		
Val	Lys	Ile	Lys	Asn	Tyr	Ser	Thr	Tyr	Ala	Gly	Asp	Val	Lys	Leu	Ala	
				420					425					430		
Tyr	Arg	Leu	Thr	Leu	Pro	Asn	Gly	Thr	Glu	Thr	Thr	Asn	Pro	Ala	Val	
				435					440					445		
Thr	Val	Pro	Ile	Val	Trp	Glu	Asp	Ile	Ile	Gly	Glu	Ser	Thr	Gly	Asn	
				450					455					460		
Ile	Thr	Ile	Pro	Cys	Ser	Gln	Phe	Ala	Glu	Gly	Lys	Asn	Thr	Ile	Ser	
465					470					475					480	
Ile	Leu	Tyr	Arg	Thr	Asp	Gly	Met	Ala	Asp	Trp	Lys	Glu	Leu	Lys	His	
				485					490					495		

Leu Ile Thr Asp Leu Ser Ser Ser Asp Ile Ala Gly Lys Asp Val Ser
755 760 765

Thr Ile Val Leu Tyr Pro Asn Pro Ala His Asp Tyr Val His Val Ala
770 775 780

Ile Pro Pro Thr Tyr Ala Gly Ser Thr Leu Arg Leu Phe Asp Ile Gln
785 790 795 800

Gly Arg Met Gln Leu Ser Thr Lys Ile Glu Ser Ala Asp Met Arg Leu
805 810 815

Asp Val Glu Arg Leu Pro Lys Gly Thr Tyr Ile Val Val Val Glu Asp
820 825 830

Met Val Gly Lys Leu Phe Ile Arg
835 840

<210> 6

<211> 398

<212> PRT

<213> Streptococcus pyogenes

<400> 6

Met Asn Lys Lys Lys Leu Gly Ile Arg Leu Leu Ser Leu Leu Ala Leu
1 5 10 15

Gly Gly Phe Val Leu Ala Asn Pro Val Phe Ala Asp Gln Asn Phe Ala
20 25 30

Arg Asn Glu Lys Glu Ala Lys Asp Ser Ala Ile Thr Phe Ile Gln Lys
35 40 45

Ser Ala Ala Ile Lys Ala Gly Ala Arg Ser Ala Glu Asp Ile Lys Leu
50 55 60

Asp Lys Val Asn Leu Gly Gly Glu Leu Ser Gly Ser Asn Met Tyr Val
65 70 75 80

Tyr Asn Ile Ser Thr Gly Gly Phe Val Ile Val Ser Gly Asp Lys Arg
85 90 95

Ser Pro Glu Ile Leu Gly Tyr Ser Thr Ser Gly Ser Phe Asp Ala Asn
100 105 110

Gly Lys Glu Asn Ile Ala Ser Phe Met Glu Ser Tyr Val Glu Gln Ile
115 120 125

TOPOT DEEDOT

Lys Glu Asn Lys Lys Leu Asp Thr Thr Tyr Ala Gly Thr Ala Glu Ile
130 135 140

Lys Gln Pro Val Val Lys Ser Leu Leu Asp Ser Lys Gly Ile His Tyr
145 150 155 160

Asn Gln Gly Asn Pro Tyr Asn Leu Leu Thr Pro Val Ile Glu Lys Val
165 170 175

Lys Pro Gly Glu Gln Ser Phe Val Gly Gln His Ala Ala Thr Gly Cys
180 185 190

Val Ala Thr Ala Thr Ala Gln Ile Met Lys Tyr His Asn Tyr Pro Asn
195 200 205

Lys Gly Leu Lys Asp Tyr Thr Tyr Thr Leu Ser Ser Asn Asn Pro Tyr
210 215 220

Phe Asn His Pro Lys Asn Leu Phe Ala Ala Ile Ser Thr Arg Gln Tyr
225 230 235 240

Asn Trp Asn Asn Ile Leu Pro Thr Tyr Ser Gly Arg Glu Ser Asn Val
245 250 255

Gln Lys Met Ala Ile Ser Glu Leu Met Ala Asp Val Gly Ile Ser Val
260 265 270

Asp Met Asp Tyr Gly Pro Ser Ser Gly Ser Ala Gly Ser Ser Arg Val
275 280 285

Gln Arg Ala Leu Lys Glu Asn Phe Gly Tyr Asn Gln Ser Val His Gln
290 295 300

Ile Asn Arg Ser Asp Phe Ser Lys Gln Asp Trp Glu Ala Gln Ile Asp
305 310 315 320

Lys Glu Leu Ser Gln Asn Gln Pro Val Tyr Tyr Gln Gly Val Gly Lys
325 330 335

Val Gly Gly His Ala Phe Val Ile Asp Gly Ala Asp Gly Arg Asn Phe
340 345 350

Tyr His Val Asn Trp Gly Trp Gly Gly Val Ser Asp Gly Phe Phe Arg
355 360 365

Leu Asp Ala Leu Asn Pro Ser Ala Leu Gly Thr Gly Gly Gly Ala Gly
370 375 380

Gly Phe Asn Gly Tyr Gln Ser Ala Val Val Gly Ile Lys Pro
385 390 395

10030330.101901